

IN THE CLAIMS:

Please amend the claims as follows:

12 (once amended). A method for studying lipid metabolism comprising obtaining a first animal defined by claim 1, and detecting [the] a phenotype of said first animal that is caused by the expression or mis-expression of said SREBP-pathway protein [in the animal of Claim 1].

13 (once amended). The method of Claim 12 additionally comprising observing a phenotype of a second animal [having] that has the same genetic modification as the first animal [of Claim 1 which causes said expression or mis-expression of said SREBP pathway protein, and wherein said second animal additionally comprises] and that additionally has a mutation in a gene of interest, wherein differences, if any, between the phenotype of the first animal [of Claim 1] and the phenotype of the second animal identifies the gene of interest as capable of modifying the function of the gene encoding said SREBP pathway protein.

REMARKS

The specification has been amended pursuant to 37 C.F.R. § 1.821(d) to incorporate the Sequence Listing and the sequence identifiers corresponding to the Sequence Listing submitted concurrently herewith. The incorporation of the sequence identifiers introduces no new matter.

Claims 1-33 are currently pending. Claims 12 and 13 have been amended to more particularly point out and distinctly claim the present invention. Specifically, claim 12 has been amended to recite that the method for studying lipid metabolism comprises obtaining a first animal defined by claim 1, and detecting a phenotype of said first animal that is caused by the expression or mis-expression of said SREBP-pathway protein. Support for the amendment to claim 12 is found in the specification, *inter alia*, at page 5, line 33 to page 6, line 10 and page 29, lines 15-30. Claim 13 has been amended to recite that the method of claim 12 additionally comprises observing a phenotype of a second animal that has the same genetic modification as the first animal and that additionally has a mutation in a gene of interest, wherein differences, if any, between the phenotype of the first animal and the phenotype of the second animal identifies the gene of interest as capable of modifying the